



## SEQUENCE LISTING

> Schwab, M.  
Chen, M.

<120> NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO  
GENES AND METHODS BASED THEREON

<130> 10200-003-999

<140> 09/830,972

<141> 2001-09-24

<150> PCT/US99/26160

<151> 1999-11-05

<150> 60/107,446

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Phe Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe	
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Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Pro Leu Leu Asp 65 70 75 80	
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Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser 115 120 125	
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Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu 165 170 175	
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu 180 185 190	
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1 5 10 15

<210> 6  
<211> 9  
<212> PRT  
<213> Bos sp.

<220>  
<221> VARIANT  
<222> 2,5  
<223> Xaa = any amino acid

<400> 6  
Lys Xaa Phe Glu Xaa Val Trp Glu Val  
1 5

<210> 7  
<211> 11  
<212> PRT  
<213> Bos sp.

<400> 7  
Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys  
1 5 10

<210> 8  
<211> 16  
<212> PRT  
<213> Bos sp.

<400> 8  
Lys Ala Val Ala Ala Glu Ala Ser Met Arg Glu Glu Tyr Ala Asp Phe  
1 5 10 15

<210> 9  
<211> 13  
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<213> Bos sp.

<400> 9  
Glu Tyr Leu Gly Asp Leu Pro Ala Val Leu Pro Thr Glu  
1 5 10

<210> 10  
<211> 12  
<212> PRT

92

<213> Bos sp.

<400> 10

Glu Ile Ala Asp Ile Gln Asp Gly Ala Gly Ser Leu  
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<210> 11

<211> 15

<212> PRT

<213> Bos sp.

<400> 11

Lys Pro Tyr Leu Glu Ser Phe Gln Pro Ser Leu Gly Ile Thr Lys  
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<210> 12

<211> 9

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<213> Bos sp.

<400> 12

Lys Pro Phe Glu Arg Val Trp Glu Val  
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<211> 11

<212> PRT

<213> Bos sp.

<400> 13

Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys  
1 5 10

<210> 14

<211> 16

<212> PRT

<213> Bos sp.

<400> 14

Lys Gly Val Ala Ala Glu Ala Ser Met Gly Glu Glu Tyr Ala Asp Phe  
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<210> 15

<211> 13

<212> PRT

<213> Rattus sp.

<400> 15

Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu  
1 5 10

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<213> Rattus sp.

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Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys  
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<212> PRT  
<213> Rattus sp.

<400> 18  
Lys Pro Phe Glu Gln Ala Trp Glu Val  
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<210> 19  
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<400> 19  
Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys  
1 5 10

<210> 20  
<211> 16  
<212> PRT  
<213> Rattus sp.

<400> 20  
Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe  
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<210> 21  
<211> 186  
<212> PRT  
<213> Homo sapiens

<400> 21  
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly  
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Ser Phe Leu Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser  
20 25 30  
Val Val Ala Tyr Leu Ala Leu Ala Leu Ser Ala Thr Ile Ser Phe  
35 40 45  
Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly  
50 55 60  
His Pro Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu  
65 70 75 80  
Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr  
85 90 95  
Leu Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser  
100 105 110  
Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu  
115 120 125  
Phe Asn Gly Leu Thr Leu Leu Met Ala Val Val Ser Met Phe Thr  
130 135 140  
Leu Pro Val Val Tyr Val Lys His Gln Ala Gln Ile Asp Gln Tyr Leu  
145 150 155 160  
Gly Leu Val Arg Thr His Ile Asn Ala Val Val Ala Lys Ile Gln Ala  
165 170 175

Lys Ile Pro Gly Ala Lys Arg His Ala Glu  
180 185

<210> 22  
<211> 186  
<212> PRT  
<213> Rattus sp.

<400> 22

Asp Leu Leu Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly  
1 5 10 15  
Ser Phe Leu Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser  
20 25 30  
Val Val Ala Tyr Leu Ala Leu Ala Leu Ser Ala Thr Ile Ser Phe  
35 40 45  
Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly  
50 55 60  
His Pro Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu  
65 70 75 80  
Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Leu Tyr Val Asn Ser Thr  
85 90 95  
Leu Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser  
100 105 110  
Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu  
115 120 125  
Phe Asn Gly Leu Thr Leu Leu Leu Met Ala Val Val Ser Met Phe Thr  
130 135 140  
Leu Pro Val Val Tyr Val Lys His Gln Ala Gln Val Asp Gln Tyr Leu  
145 150 155 160  
Gly Leu Val Arg Thr His Ile Asn Thr Val Val Ala Lys Ile Gln Ala  
165 170 175  
Lys Ile Pro Gly Ala Lys Arg His Ala Glu  
180 185

<210> 23  
<211> 186  
<212> PRT  
<213> Gallus gallus

<400> 23

Asn Leu Leu Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly  
1 5 10 15  
Ser Leu Leu Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser  
20 25 30  
Val Val Ala Tyr Leu Ala Leu Ala Gly Leu Ser Ala Thr Ile Ser Phe  
35 40 45  
Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly  
50 55 60  
His Pro Phe Lys Ala Tyr Leu Asp Met Glu Met Asn Leu Ser Gln Asp  
65 70 75 80  
Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Leu Tyr Val Asn Ser Thr  
85 90 95  
Val Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser  
100 105 110  
Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu  
115 120 125  
Phe Asn Gly Leu Thr Leu Leu Ile Met Ala Val Val Ser Met Phe Thr  
130 135 140  
Leu Pro Val Val Tyr Asp Lys Tyr Gln Ala Gln Ile Asp Gln Tyr Leu  
145 150 155 160  
Gly Leu Val Arg Thr His Ile Asn Thr Val Val Ala Lys Ile Gln Ala  
165 170 175

Lys Ile Pro Gly Ala Lys Arg Lys Ala Glu  
180 185

<210> 24  
<211> 186  
<212> PRT  
<213> Bos sp.

<400> 24

Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly  
1 5 10 15  
Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser  
20 25 30  
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe  
35 40 45  
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly  
50 55 60  
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu  
65 70 75 80  
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr  
85 90 95  
Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser  
100 105 110  
Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu  
115 120 125  
Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser  
130 135 140  
Val Pro Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu  
145 150 155 160  
Gly Leu Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala  
165 170 175  
Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu  
180 185

<210> 25  
<211> 186  
<212> PRT  
<213> Rattus sp.

<400> 25

Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly  
1 5 10 15  
Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser  
20 25 30  
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe  
35 40 45  
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly  
50 55 60  
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu  
65 70 75 80  
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser Thr  
85 90 95  
Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser  
100 105 110  
Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu  
115 120 125  
Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser  
130 135 140  
Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr Leu  
145 150 155 160  
Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln Ala  
165 170 175

Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp  
180 185

<210> 26  
<211> 194  
<212> PRT  
<213> C. elegans

<400> 26

Asp Val Ile Tyr Trp Arg Asp Ala Lys Lys Ser Ala Ile Val Leu Ser  
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Leu Ala Leu Leu Val Leu Phe Val Leu Ala Lys Tyr Pro Leu Leu Thr  
20 25 30  
Val Val Thr Tyr Ser Leu Leu Leu Ala Leu Gly Ala Ala Gly Phe  
35 40 45  
Arg Val Phe Lys Lys Val Glu Ala Gln Ile Lys Lys Thr Asp Ser Glu  
50 55 60  
His Pro Phe Ser Glu Ile Leu Ala Gln Asp Leu Thr Leu Pro Gln Glu  
65 70 75 80  
Lys Val His Ala Gln Ala Asp Val Phe Val Glu His Ala Thr Cys Ile  
85 90 95  
Ala Asn Lys Leu Lys Lys Leu Val Phe Val Glu Ser Pro Leu Glu Ser  
100 105 110  
Ile Lys Phe Gly Leu Val Leu Trp Ser Leu Thr Tyr Ile Ala Ser Trp  
115 120 125  
Phe Ser Gly Phe Thr Leu Ala Ile Leu Gly Leu Leu Gly Val Phe Ser  
130 135 140  
Val Pro Lys Val Tyr Glu Ser Asn Gln Glu Ala Ile Asp Pro His Leu  
145 150 155 160  
Ala Thr Ile Ser Gly His Leu Lys Asn Val Gln Asn Ile Ile Asp Glu  
165 170 175  
Lys Leu Pro Phe Leu Arg Ser Ala Pro Val Ala Ala Glu Glu Lys Lys  
180 185 190  
Asp Gln

<210> 27  
<211> 150  
<212> PRT  
<213> D. melanogaster

<400> 27

Asn Leu Leu Leu Trp Arg Asn Ser Arg Lys Thr Leu Ile Val Phe Thr  
1 5 10 15  
Gly Ile Leu Leu Leu Leu Asp Val Met Val His Ser Val Ile Ser  
20 25 30  
Val Ile Ser Met Val Gly Ile Thr Val Leu Ile Ala Ala Ile Gly His  
35 40 45  
Arg Leu Leu Val Gln Phe Trp Ser Ile Trp Lys Lys Asp Glu Asn Lys  
50 55 60  
Asp Gln Ile Leu Arg Phe Tyr Pro His Pro Lys Ile Glu Ile Pro Arg  
65 70 75 80  
Glu Glu Thr Leu Tyr Leu Ala Gly Lys Ala Val Ser His Ile Asn Leu  
85 90 95  
Ile Leu Asn Arg Met Ile Glu Leu Leu Leu Val Glu Lys Trp Glu Asp  
100 105 110  
Ser Leu Lys Phe Leu Val Leu Leu Cys Gly Ile Asn Leu Leu Gly Asp  
115 120 125  
Cys Phe Asn Gly Leu Thr Leu Ile Phe Gly Met Cys Ile Cys Cys  
130 135 140  
Leu Thr Leu Leu Tyr Leu  
145 150

<210> 28  
<211> 3833  
<212> DNA  
<213> Bos sp.

<400> 28

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cgattttatac	aattgtgggt	taagctgtat	tgaactaaat	ctgtggaatg	cattgtgaac	3780
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<210> 29

<211> 1178

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(1178) at all Xaa position

<223> Xaa = any amino acid

<400> 29

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Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp  
35 40 45  
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Gly Leu Ser  
50 55 60  
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp  
65 70 75 80  
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala  
85 90 95  
Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro  
100 105 110  
Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Val  
115 120 125  
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro  
130 135 140  
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr  
145 150 155 160  
Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro  
165 170 175  
Lys Arg Arg Gly Ser Ser Gly Ala Val Val Xaa Xaa Xaa Xaa Lys Ile  
180 185 190  
Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu  
195 200 205  
Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Xaa Pro Ser Leu  
210 215 220  
Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn  
225 230 235 240  
Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser  
245 250 255  
Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp  
260 265 270  
Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser  
275 280 285  
Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn  
290 295 300  
Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu  
305 310 315 320  
Val Ser Asn Asn Ile Leu His Xaa Gln Gln Glu Leu Pro Thr Ala Leu  
325 330 335



Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys  
 340 345 350  
 Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu  
 355 360 365  
 Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp  
 370 375 380  
 Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser  
 385 390 395 400  
 Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu  
 405 410 415  
 Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser  
 420 425 430  
 Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile  
 435 440 445  
 Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn  
 450 455 460  
 Ile Phe Pro Leu Leu Glu Asp Pro Thr Ser Glu Asn Xaa Thr Asp Glu  
 465 470 475 480  
 Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr  
 485 490 495  
 Ser Thr Lys Thr Ser Asn Pro Phe Phe Val Ala Ala Gln Asp Ser Glu  
 500 505 510  
 Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val  
 515 520 525  
 Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala  
 530 535 540  
 Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu  
 545 550 555 560  
 Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu  
 565 570 575  
 Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr  
 580 585 590  
 Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser  
 595 600 605  
 Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro  
 610 615 620  
 Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu  
 625 630 635 640  
 Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Val Ser  
 645 650 655  
 Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu  
 660 665 670  
 Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys  
 675 680 685  
 Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser  
 690 695 700  
 Glu Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val  
 705 710 715 720  
 Glu Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp  
 725 730 735  
 Ser Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val  
 740 745 750  
 Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu  
 755 760 765  
 Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr  
 770 775 780  
 Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu  
 785 790 795 800  
 Pro Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln  
 805 810 815  
 Met Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile  
 820 825 830

Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser  
 835 840 845  
 Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr  
 850 855 860  
 Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser  
 865 870 875 880  
 His Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro  
 885 890 895  
 Cys Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys  
 900 905 910  
 Val Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser  
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 Ala Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Gly  
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 His Thr Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Glu  
 945 950 955 960  
 Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg  
 965 970 975  
 Ser Pro Ser Ala Ile Phe Ser Ala Asp Leu Gly Lys Thr Ser Val Val  
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 Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly  
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 Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser  
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 Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe  
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 Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly  
 1045 1050 1055  
 His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu  
 1060 1065 1070  
 Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr  
 1075 1080 1085  
 Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser  
 1090 1095 1100  
 Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu  
 1105 1110 1115 1120  
 Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser  
 1125 1130 1135  
 Val Pro Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu  
 1140 1145 1150  
 Gly Leu Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala  
 1155 1160 1165  
 Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu  
 1170 1175

<210> 30  
 <211> 1163  
 <212> PRT  
 <213> Rattus sp.

<220>  
 <221> VARIANT  
 <222> (1)...(1163) at all Xaa position  
 <223> Xaa = any amino acid

<400> 30  
 Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser  
 1 5 10 15  
 Pro Pro Arg Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro  
 20 25 30  
 Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp  
 35 40 45

18-9

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly  
 50 55 60  
 Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Pro Leu Leu Asp  
 65 70 75 80  
 Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala  
 85 90 95  
 Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro  
 100 105 110  
 Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser  
 115 120 125  
 Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro  
 130 135 140  
 Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr  
 145 150 155 160  
 Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu  
 165 170 175  
 Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu  
 180 185 190  
 Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly  
 195 200 205  
 Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro  
 210 215 220  
 Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu  
 225 230 235 240  
 Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr  
 245 250 255  
 Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe  
 260 265 270  
 Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met  
 275 280 285  
 Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val  
 290 295 300  
 Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp  
 305 310 315 320  
 Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly  
 325 330 335  
 Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn  
 340 345 350  
 Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp  
 355 360 365  
 Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly  
 370 375 380  
 Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp  
 385 390 395 400  
 Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp  
 405 410 415  
 Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro  
 420 425 430  
 Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser  
 435 440 445  
 Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His  
 450 455 460  
 Thr Ser Glu Asn Xaa Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala  
 465 470 475 480  
 Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu  
 485 490 495  
 Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu  
 500 505 510  
 Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr  
 515 520 525  
 Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr  
 530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser  
 545 550 555 560  
 Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser  
 565 570 575  
 Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
 580 585 590  
 Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val  
 595 600 605  
 Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Val Ser Tyr  
 610 615 620  
 Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala  
 625 630 635 640  
 Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu  
 645 650 655  
 Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile  
 660 665 670  
 Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro  
 675 680 685  
 Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser  
 690 695 700  
 Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Pro Glu Ser Glu  
 705 710 715 720  
 Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr  
 725 730 735  
 Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser  
 740 745 750  
 Glu Thr Val Ala Gln His Lys Glu Arg Leu Ser Ala Ser Pro Gln  
 755 760 765  
 Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser  
 770 775 780  
 Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu  
 785 790 795 800  
 Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn  
 805 810 815  
 Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr  
 820 825 830  
 Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe  
 835 840 845  
 Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp  
 850 855 860  
 Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala  
 865 870 875 880  
 Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn  
 885 890 895  
 Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn  
 900 905 910  
 Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala  
 915 920 925  
 Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu  
 930 935 940  
 Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp  
 945 950 955 960  
 Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val  
 965 970 975  
 Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe  
 980 985 990  
 Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val  
 995 1000 1005  
 Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser  
 1010 1015 1020  
 Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu  
 1025 1030 1035 1040

Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu  
 1045 1050 1055  
 Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser  
 1060 1065 1070  
 Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp  
 1075 1080 1085  
 Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala  
 1090 1095 1100  
 Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe  
 1105 1110 1115 1120  
 Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr  
 1125 1130 1135  
 Leu Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln  
 1140 1145 1150  
 Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp  
 1155 1160

<210> 31  
 <211> 1568  
 <212> DNA  
 <213> Rattus sp.

<400> 31  
 caggcttagt ctggggaagc ggggtgtttca tgtctcaggg agaattttgc agtttacagc 60  
 gtttctgttg gtatgcataa tttgtaattg ctgctggagg gcagatcgtg gcaagaaatg 120  
 gacggacaga agaaacattg gaaggacaag gttgttgacc tctctactg gagagacatt 180  
 aagaagactg gagtggtgtt tgggtgccagc ttattcctgc tgcgtgtctt gacagtgttc 240  
 agcattgtca gtgtaacggc ctacattgcc ttggccctgc tctcgggtgac tatcagcttt 300  
 aggatataata agggcgtgat ccaggctatc cagaaatcag atgaaggcca cccattcagg 360  
 gcatatttag aatctgaagt tgctatatca gaggaattgg ttcagaaata cagtaattct 420  
 gctcttggtc atgtgaacag cacaataaaa gaactgaggc ggcttttctt agttgatgat 480  
 ttagttgatt ccctgaagtt tgcagtggtg atgtgggtgt ttacttatgt tgggtgccttg 540  
 ttcaatggtc tgacactact gatttttagct ctgatctcac tcttcagtat tctgttatt 600  
 tatgaacggc atcaggtgca gatagatcat tatctaggac ttgcaaaca gagtgtaag 660  
 gatgccatgg ccaaaatcca agcaaaaatc cctggattga agcgcaaagc agattgaaaa 720  
 agccccaac agaagttcat ctttaaaggg gacactcact tgattacggg ggtgggaggt 780  
 caggggtgag cccttggttg ccgtgcggtt tcagctcttt attttttagca gtgcactgtt 840  
 tgaggaaaaa ttacctgtct tgacttcctg tgtttatcat ctttaagtatt gtaagctgct 900  
 gtgtatggat ctcatgttag tcacacttgt cttccccaat gaggcgcctg gtgaataaag 960  
 gactcgggga aagctgtgca ttgtatctgc tgcagggtag tctagctgta tgcagagagt 1020  
 tgtaagaag gcaaactctg gggcaggga aaccctttt acagtgtact gtgtttggtc 1080  
 agtgtaaaac tgatgcagat ttttctgaaa tgaaatgttt agatgagagc atactactaa 1140  
 agcagagtgg aaaactctgt ctttatgggtg tgttctaggt gtattgtgaa tttactgtta 1200  
 tattgccaat ataagtaa atagacctaa tctatatata gtgtttcaca aagcttagat 1260  
 ctttaacctt gcagctgccc cacagtgcct gacctctgag tcattgggta tgcagtgtag 1320  
 tcccaagcac ataaactagg aagagaaatg tattttagtg agtgctacct accacctgtt 1380  
 ttcaagaaaa tatagaactc caacaaaaat atagaatgct atttcaaaga cttactgtat 1440  
 gtatagttaa ttttgtcaca gactctgaaa ttctatggac tgaatttcat gcttccaaat 1500  
 gtttgcagtt atcaaacatt gttatgcaag aaatcataaa atgaagactt ataccattgt 1560  
 ggtttaag 1568

<210> 32  
 <211> 141  
 <212> PRT  
 <213> Rattus sp.

<400> 32  
 Gln Ala Ser Gly Glu Ala Gly Val Ser Cys Leu Arg Glu Asn Phe Ala  
 1 5 10 15  
 Val Tyr Ser Val Ser Val Gly Met His Asn Leu Leu Leu Leu Gly  
 20 25 30  
 Arg Ser Trp Gln Glu Met Asp Gly Gln Lys Lys His Trp Lys Asp Lys

AL

35 40 45  
 Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val  
 50 55 60  
 Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile  
 65 70 75 80  
 Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile  
 85 90 95  
 Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Ala Lys Ser Asp  
 100 105 110  
 Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser  
 115 120 125  
 Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly  
 130 135 140

<210> 33  
 <211> 18  
 <212> PRT  
 <213> Bos sp.

<400> 33  
 Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu  
 1 5 10 15  
 Glu Ala

<210> 34  
 <211> 13  
 <212> DNA  
 <213> Homo sapiens

<400> 34  
 gccgcccrrcca tgg 13

<210> 35  
 <211> 248  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)... (248) at all n positions  
 <223> n=a, c, g or t

<400> 35  
 gagccgtcac cacagtaggt ccctcggctc agtcggccca gcccctctca gtcctcccca 60  
 acccccacaa ccgcccgcgc tctgagacg cgccccggcg gcggcgggcan agctgcagca 120  
 tcattctccac cctccagcca tggaagacct ggaccagtct cctctggtct cgtcctcggga 180  
 cagcccacccc cggccgcagc ccgcgttcaa gtaccagttc gtgaggggagc ccgaggacga 240  
 ggaggaag 248

<210> 36  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)... (36) at all n positions  
 <223> n=a, c, g or t

<400> 36  
 gaaaatatgg acttgaagga gcagccaggt aacactatatt cggtctggtca agaggatttc 60

ccatctgtcc	tgcttgaaac	tgctgcttct	nttccttctc	tgtctcctct	ctcagccgct	120
tctttcaaag	aacatgaata	ccttggtaat	ttgtcaacag	tattacccac	tgaaggaaca	180
cttcaagaaa	atgtcagtga	agcttctaaa	gaggctctcag	agaaggcaaa	aactctactc	240
atagatagag	atttaacaga	gttttcagaa	ttaggaatac	tcagaaatgg	gatcatcggt	300
cagtgtctct	ccaaaagcag	aatctgccgt	aaatagtagg	caaatcctag	gggaagaaat	360
aattcgtgga	aaaataaag					379

<210> 37  
 <211> 281  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (1)... (281) at all n positions  
 <223> n=a, c, g or t

<400> 37	
gatagagatt	taacagagtt
gtctctccaa	aagcagaatc
aaaaataaag	atgaagaaga
ttacctacag	ctcttactaa
aaagacagtt	ttatgaaaga
ttcagaatta	gaatactcag
tgccgtaata	gtagcaaatac
gaagttagtt	agtaataaca
attggttaaa	gaggatgaag
gagttgcagt	ggaantcctt
g	
	60
	120
	180
	240
	281

<210> 38  
 <211> 640  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (1)... (640) at all n positions  
 <223> n=a, c, g or t

<400> 38	
ttaaagagga	tgaagttgtg
ttgcagtgga	agctcctatg
gggaagtga	agatagtaag
gcaacttgga	aagtaaagtg
acgaaaaga	tagtgagagt
taaaggatcg	ttcaggagca
gcattgcaac	naacattttt
aaaaaataga	agaaaagaag
cctttcttgt	gcagcacagg
agantcttgc	aacatcctga
ttctggtcaa	gtnntttgan
tcttcagaaa	aagcaaaaaga
agggaggaat	atgcagactt
atagttggc	tgctggagggt
gttttgcaga	tagccttgag
atacttcttt	ccccagtagc
gtgctccctt	taaccagca
agatcctact	tcagaaaatt
accgagaaga	atactagcac
gatatgtccc	acgnttatta
gattgttccn	gagctttgaa
gtcactcgtat	
	60
	120
	180
	240
	300
	360
	420
	480
	540
	600
	640

<210> 39  
 <211> 346  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (1)... (346) at all n positions  
 <223> n=a, c, g or t

<400> 39	
ctgtgcccg	ccccacccc
gaggggttag	ctgcaccgcc
gtactccctg	caccgtctca
tgtatatatt	tgtatgtnac
tggttcagatg	tcccccactg
ttacctctcc	ctaaggctgc
atattatatt	tggtctcagg
tggttaaaatg	agttcctacc
agggctgagg	ggcctgcgcc
cagagctggc	
	60
	120
	180
	240

ctcccncaac	acctgctgcg	cttggttaggt	gtgggtggcgt	tatggcagcc	eggctgctgc	300
ttggatgcca	gnttggncct	gggccggtgc	tggggggcac	agttgt		346

<210> 40  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<400> 40						
gtggcacaac	tgcctgaagg	cctgactcca	gatttagtac	aggaagcatg	tgaaagtga	60
ttgaatgaag	ttactggtag	aaagattgct	tatgaaacaa	aatggacttg	gttcaaacat	120
cagaagttat	gcaagagtca	ctctatcctg	cagcacagct	ttgcccatca	tttgaagagt	180
cagaagctac	tccttcacca	gttttgccctg	acattgttat	ggaagcacca	ttgaattctg	240
cagttcctag	tgctgggtgct	tccgtgatac	agcccagctc	atcaccatta	gaggcttctt	300
cagttaatta	tgaagcataa	acatg				325

<210> 41  
 <211> 338  
 <212> DNA  
 <213> Homo sapiens



<400> 41						
gcatgtgaaa	gtgaattgaa	tgaagttact	ggtacaaaga	ttgcttatga	aacaaaaatg	60
gacttggttc	aaacatcaga	agttatgcaa	gagtcactct	atcctgcagc	acagctttgc	120
ccatcatttg	aagagtcaga	agctactcct	tcaccagttt	tgcttgacat	tgttatggaa	180
gcaccattga	attctgcagt	tcctagtgtc	ggtgcttccg	tgatacagcc	cagctcatca	240
ccattagaag	cttcttcagt	taattatgaa	agcataaaac	atgagcctga	aaacccccca	300
ccatatgaag	aggccatgag	tgtatcacta	aaaaaagt			338

<210> 42  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)... (480) at all n positions  
 <223> n=a, c, g or t

<400> 42						
aagactggag	tggtgttttg	tgccagccta	ttcctgctgc	tttcattgac	agtattcagc	60
attgtgagcg	taacagccta	cattgccttg	gccctgctct	ctgtgaccat	cagctttagg	120
atatacaagg	gtgtgatcca	agctatccag	aaatcagatg	aaggccaccc	attcagggca	180
tatctggaat	ctgaagttgc	tatatctgag	gagttgggtc	agaagtacag	taattctgct	240
cttggtcatg	tgaactgcac	gataaaggaa	ctcaggcgcc	tcttcttagt	tgatgattta	300
gttgattctc	tgaagtttgc	agtgttgatg	tgggtattta	cctatgttgg	tgccctgttt	360
aatggctctg	cactactgat	ttnggctctc	attccactcc	tncaagtgtt	cctgggtattt	420
ntgaacggca	tcnnggcacag	ntagatcatt	atccaggact	tgcaaatagg	aatgtaaaga	480

<210> 43  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 43												
Met	Glu	Asp	Leu	Asp	Gln	Ser	Pro	Leu	Val	Ser	Ser	Ser
1				5					10			

<210> 44  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens





<400> 44  
Lys Ile Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly  
1 5 10 15

<210> 45  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 45  
Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser Phe Asn  
1 5 10 15  
Glu Lys Arg

<210> 46  
<211> 50  
<212> PRT  
<213> Homo sapiens

AA  
<400> 46  
Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu  
1 5 10 15  
Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala  
20 25 30  
Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro  
35 40 45  
Ser Ser  
50

<210> 47  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> degenerate oligonucleotides designed from the bovine NI220  
peptide 1 sequence

<220>  
<221> modified base  
<222> (1)... (26) at all n positions  
<223> n=inosine

<400> 47  
tcngtnggya anacngcngg yaartc 26

<210> 48  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> degenerate oligonucleotides designed from the bovine NI220  
peptide 1 sequence

<220>  
<221> modified base  
<222> (1)... (23) at all n positions  
<223> n=inosine

<400> 48

25

tcngtnggna gnacnggyaa ytc

23

<210> 49  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> degenerate oligonucleotides designed from the bovine NI220  
peptide 1 sequence

<220>  
<221> modified base  
<222> (1)... (25) at all n positions  
<223> n=inosine

<400> 49  
tcngtnggya anacngcggn agrtc

25

<210> 50  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> degenerate oligonucleotides designed from the bovine NI220  
peptide 1 sequence

<220>  
<221> modified base  
<222> (1)... (26) at all n positions  
<223> n=inosine

<400> 50  
tcngtnggna gnacngcngg nagrtc

26

<210> 51  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> degenerate oligonucleotides designed from the bovine NI220  
peptide 2 sequence

<220>  
<221> modified base  
<222> (1)... (26) at all n positions  
<223> n=inosine

<400> 51  
garathgcng anathcarga yggnga

26

27